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RAW SEQUENCE LISTING  
PATENT APPLICATION: -US/10/042,431

DATE: 01/27/2002  
TIME: 15:34:20

Input Set : A:\101476ul.app  
Output Set: N:\CRF3\01272002\J042431.raw

ENTERED

3 <110> APPLICANT: MCCARTHY, Sean A  
4 BARNES, Thomas M  
5 FRASER, Christopher C  
6 SHARP, John D  
8 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,  
9 PREVENTIVE, THERAPEUTIC, AND OTHER USES  
11 <130> FILE REFERENCE: 10147-6U2  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/042,431  
14 <141> CURRENT FILING DATE: 2001-10-25  
16 <150> PRIOR APPLICATION NUMBER: US 09/333,159  
17 <151> PRIOR FILING DATE: 1999-06-14  
19 <150> PRIOR APPLICATION NUMBER: US 09/578,063  
20 <151> PRIOR FILING DATE: 2000-05-24  
22 <160> NUMBER OF SEQ ID NOS: 79  
24 <170> SOFTWARE: PatentIn Ver. 2.1  
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28 <212> TYPE: DNA  
29 <213> ORGANISM: Homo sapiens  
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34 ccgcgcgcgc agtgtttcac agccaatggt cgcggattata ggggaacaca gaactggaca 180  
35 gcactacaag gcgggaagcc atgtctgttt tggaaacgaga ctttcacgca tccaatacaac 240  
36 actctgaaat accccaacgc ggaggggggc ctgggtgagc acaactattg cagaatacca 300  
37 gatggagacg tgagccctcg gtgctatgt gcagagcagc ggaacacttg ctactggaag 360  
38 tactgtgaga tactctgttg ccagatgcct ggaaaccttg gctgtacaaa ggaatcatga 420  
39 aacccaacgc ctctaactgg caccagtaaa acgtccaaca aactcaccat acaaaacttcg 480  
40 atcagttttt gtcggagtcg gagggtcaag ttgctggga tggagtcagg ctatgcttgc 540  
41 ttctgtggaa acaactctga ttactggaag tacggggagg cagccagtag cgaatgcaac 600  
42 agcgtctgct tcggggatca caccacaacc tctgtgggac tactcagcca tgtcttctgt 660  
43 gatactctcg tgggcgcctg cgggtgggac tactcagcca tgtcttctgt ggtctattcc 720  
44 cctgacttcg ccgacaccta tgccacgggg aggggtctgt actggaccat ccgggttccg 780  
45 ggggcctccc acatccactt cagcttcccc ctatttgaca gcttcacagg ggcgggacat 840  
46 gtggagcttc tggatggcta caaccaacgt gtcttagccc gcttcacagg caactctcgt 900  
47 ccaactctgt octtcaacgt ctctctggac ttctgcatct tgtatttctt gctctgctgc 960  
48 atcaatcagg cccagggatt tgcgtgttta taccagccgc tcaagggaag actgcacagc 1020  
49 gagagggccc cgtgcaacca cagcgtggcc gatgtgatca cggagcagcc caactctcgt 1080  
50 ctgacgcgtg ccggtctctc caaagtctct tatgtcatca ccaccagccc cagccaccca 1140  
51 cctcagactg tcccaggtag caattctctg gcgccaccca tggggctctg aagccacaga 1200  
52 gttgaaggat ggacagctca ttggtctggca actctcctca tctctcagat cacagccatt 1260  
53 gtacgaaaga tactctcgca cgtcaccatc aaatcccatc gttgtctcgt ttcaggggac 1320  
54 cttagggatt gtcatacaac agggactctg ggggaaatct ggagcatttt ttacaagcct 1380

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55 tccacttcaa ttctcatctt taagaagaaa ctcaagggtc agagtcaaca agatgaccgc 1440
56 aatccccccttg tgagtgacta aaaaccccac tgtgcctagg acttgaggto cctcttttag 1500
57 ctcaaggctg cgtgtgttcaa cctctcctgt ggttctcttc tgacagactc ttccctcttc 1560
58 tcctctctgcc tcggcctctt cggggaaacc ctctctctac agactaggaa gaggcacctg 1620
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70 gattataggg gaacacagaa ctggacagca ctacaaggcg ggaagccatg tctgttttgg 180
71 aacgagactt tccagctatc atacaacact ctgaaatacc ccaacgggga gggggcctcg 240
72 ggtgagcaga actattgcag aaatccagat ggagactgta gccctggtg ctatgtggca 300
73 gagcagcagg atggtgtcta ctggaagatc tgtgagatag ctgcttgcca gatgctgga 360
74 aaaccttggt gctacaagga aacttgcatc agtttttgtc ggagtcagag gttcaagttt 420
75 tccaacaaac tcaccataca aacttgcatc agtttttgtc ggagtcagag gttcaagttt 480
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78 ggtggcgatg gcaggtatcat cctctttgat gctctctggt gcgctcgctg cagcgggagg 660
79 tcagccatgt ctctgttgtt ctattccctc gacttcccgc acactatgac ttcccaattt 720
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88 ctctctatcc tcacagtcac agccattgta gcaaaagata tctgacagt cacttcaaaa 1260
89 tccactgttg ttctctgttc aggggacctt agggattgtg atcaaccagg gacttcgggg 1320
90 gaaatctgga gcatttttta caagccttcc acttcaattt ccatctttaa gaagaaactc 1380
91 aagggtcaga gtcaacaaga tgacgcgaat cccctgtgta gtgac
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95 <211> LENGTH: 475
96 <212> TYPE: PRT
97 <213> ORGANISM: Homo sapiens
99 <400> SEQUENCE: 3
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101 1 5 10 15
103 Thr Leu Ala Ala Arg Pro Ala Pro Ser Pro Gly Leu Gly Pro Gly Pro
104 20 25 30
106 Glu Cys Phe Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp
107 35 40 45
109 Thr Ala Leu Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe
110 50 55 60
112 Gln His Pro Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Leu
113 65 70 75 80

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/042,431

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118 Cys Tyr Val Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu
119      100      105      110
121 Ile Pro Ala Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His
122      115      120      125
124 Gly Asn Pro Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu
125      130      135      140
127 Thr Ile Gln Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe
128 145      150      155      160
130 Ala Gly Met Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp
131      165      170      175
133 Tyr Trp Lys Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys
134      180      185      190
136 Phe Gly Asp His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu
137      195      200      205
139 Phe Asp Thr Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ser
140      210      215      220
142 Ser Val Val Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg
143 225      230      235      240
145 Val Cys Tyr Trp Thr Ile Arg Val Pro Gly Ala Ser His Ile His Phe
146      245      250      255
148 Ser Phe Pro Leu Phe Asp Ile Arg Asp Ser Ala Asp Met Val Glu Leu
149      260      265      270
151 Leu Asp Gly Tyr Thr His Arg Val Leu Ala Arg Phe His Gly Arg Ser
152      275      280      285
154 Arg Pro Pro Leu Ser Phe Asn Val Ser Leu Asp Phe Val Ile Leu Tyr
155      290      295      300
157 Phe Phe Ser Asp Arg Ile Asn Gln Ala Gln Gly Phe Ala Val Leu Tyr
158 305      310      315      320
160 Gln Ala Val Lys Glu Glu Leu Pro Gln Glu Arg Pro Ala Val Asn Gln
161      325      330      335
163 Thr Val Ala Glu Val Ile Thr Glu Gln Ala Asn Leu Ser Val Ser Ala
164      340      345      350
166 Ala Arg Ser Ser Lys Val Leu Tyr Val Ile Thr Thr Ser Pro Ser His
167      355      360      365
169 Pro Pro Gln Thr Val Pro Gly Ser Asn Ser Trp Ala Pro Pro Met Gly
170      370      375      380
172 Ala Gly Ser His Arg Val Glu Gly Trp Thr Val Tyr Gly Leu Ala Thr
173 385      390      395      400
175 Leu Leu Ile Leu Thr Val Thr Ala Ile Val Ala Lys Ile Leu Leu His
176      405      410      415
178 Val Thr Phe Lys Ser His Arg Val Pro Ala Ser Gly Asp Leu Arg Asp
179      420      425      430
181 Cys His Gln Pro Gly Thr Ser Gly Glu Ile Trp Ser Ile Phe Tyr Lys
182      435      440      445
184 Pro Ser Thr Ser Ile Ser Ile Phe Lys Lys Lys Leu Lys Gly Gln Ser
185      450      455      460
187 Gln Gln Asp Asp Arg Asn Pro Leu Val Ser Asp

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Input Set : A:\101476ul.app  
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 192 <211> LENGTH: 19  
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 194 <213> ORGANISM: Homo sapiens  
 196 <400> SEQUENCE: 4  
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 200 Thr Leu Ala  
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 205 <211> LENGTH: 456  
 206 <212> TYPE: PRT  
 207 <213> ORGANISM: Homo sapiens  
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 213 Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp Thr Ala Leu  
 214 20 25 30  
 216 Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His Pro  
 217 35 40 45  
 219 Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Leu Gly Glu His  
 220 50 55 60  
 222 Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr Val  
 223 65 70 75 80  
 225 Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro Ala  
 226 85 90 95  
 228 Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn Pro  
 229 100 105 110  
 231 Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile Gln  
 232 115 120 125  
 234 Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly Met  
 235 130 135 140  
 237 Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp Tyr Trp Lys  
 238 145 150 155 160  
 240 Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly Asp  
 241 165 170 175  
 243 His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu Phe Asp Thr  
 244 180 185 190  
 246 Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ser Ser Val Val  
 247 195 200 205  
 249 Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg Val Cys Tyr  
 250 210 215 220  
 252 Trp Thr Ile Arg Val Pro Gly Ala Ser His Ile His Phe Ser Phe Pro  
 253 225 230 235 240  
 255 Leu Phe Asp Ile Arg Asp Ser Ala Asp Met Val Glu Leu Leu Asp Gly  
 256 245 250 255  
 258 Tyr Thr His Arg Val Leu Ala Arg Phe His Gly Arg Ser Arg Pro Pro  
 259 260 265 270  
 261 Leu Ser Phe Asn Val Ser Leu Asp Phe Val Ile Leu Tyr Phe Phe Ser

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262          275          280          285
264 Asp Arg Ile Asn Gln Ala Gln Gly Phe Ala Val Leu Tyr Gln Ala Val
265          290          295          300
267 Lys Glu Glu Leu Pro Gln Glu Arg Pro Ala Val Asn Gln Thr Val Ala
268 305          310          315          320
270 Glu Val Ile Thr Glu Gln Ala Asn Leu Ser Val Ser Ala Ala Arg Ser
271          325          330          335
273 Ser Lys Val Leu Tyr Val Ile Thr Thr Ser Pro Ser His Pro Pro Gln
274          340          345          350
276 Thr Val Pro Gly Ser Asn Ser Trp Ala Pro Pro Met Gly Ala Gly Ser
277          355          360          365
279 His Arg Val Glu Gly Trp Thr Val Tyr Gly Leu Ala Thr Leu Leu Ile
280          370          375          380
282 Leu Thr Val Thr Ala Ile Val Ala Lys Ile Leu Leu His Val Thr Phe
283 385          390          395          400
285 Lys Ser His Arg Val Pro Ala Ser Gly Asp Leu Arg Asp Cys His Gln
286          405          410          415
288 Pro Gly Thr Ser Gly Glu Ile Trp Ser Ile Phe Tyr Lys Pro Ser Thr
289          420          425          430
291 Ser Ile Ser Ile Phe Lys Lys Lys Leu Lys Gly Gln Ser Gln Gln Asp
292          435          440          445
294 Asp Arg Asn Pro Leu Val Ser Asp
295          450          455
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299 <211> LENGTH: 373
300 <212> TYPE: PRT
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310 Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His Pro
311          35          40          45
313 Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Gly Leu Gly Glu His
314          50          55          60
316 Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr Val
317 65          70          75          80
319 Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro Ala
320          85          90          95
322 Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn Pro
323          100          105          110
325 Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile Gln
326          115          120          125
328 Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly Met
329          130          135          140
331 Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp Tyr Trp Lys
332 145          150          155          160
334 Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly Asp

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number